

IN THE CLAIMS

1-3. (canceled).

4. (currently amended) A method for sequencing a nucleic acids acid, the method comprising:

- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm²;
- (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by synthesising a first complementary copy of each of the template sequences, wherein said synthesising involves repeated cycles of incorporating a single nucleotide into the first complementary copy and detecting incorporation of the single nucleotide, thereby performing a first round of sequencing to generate a sequence of the first complementary copy;
- (c) removing the complementary copy of each of the template sequences from the array sequence;
- (d) performing a second round of sequencing of each of the immobilised single-stranded template nucleic acid molecules by synthesising a second complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of incorporating a single nucleotide into the second complementary copy and detecting incorporation of the single nucleotide to generate a sequence of the second complementary copy;[.] and
- (e) comparing the sequence of the first complementary copy to the sequence of the second complementary copy for the first and second rounds of sequencing of each of the immobilized single-stranded template nucleic acid molecules molecule to confirm sequencing data of each of the immobilized single-stranded

template nucleic acid molecules.

5-26. (canceled).

27. (currently amended) The method of claim 4, wherein the immobilised single-stranded template nucleic acid molecules are attached to a double stranded anchor.

28 (previously presented) The method of claim 27, wherein the double stranded anchor comprises a self complementary hairpin.

29 (previously presented) The method of claim 27, wherein the double stranded anchor comprises a recognition site for a restriction endonuclease.

30 (currently amended) The method of claim 4, wherein the 10^6 - 10^9 different template sequences templates are individually resolvable single molecules.

31 (previously presented) The method of claim 4, wherein the sequencing determination is carried out using cycles of incorporation and detection of fluorescently labeled nucleotides.

32 (currently amended) The method of claim 31, wherein the fluorescently labeled fluorescent nucleotides are detected using a microscope with total internal reflection based imaging.

33. (currently amended) The method of claim 4, wherein said synthesizing a complementary copy of the template sequences comprises employing a polymerase enzyme to synthesize a complementary sequence strand on the template strand one base at a time.

34. (new) The method of claim 4, wherein the comparing the sequence of the first complementary copy to the sequence of the second complementary copy for each of the immobilized single-stranded template nucleic acid molecules reduces random sequencing errors of the template sequences arising from the first round of sequencing.
35. (new) A method for simultaneously sequencing a complete genome comprising a plurality of different nucleic acids, the method comprising:
- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm²;
 - (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a first complementary copy of each of the template sequences, wherein said synthesising comprises repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated, thereby performing a first round of sequencing;
 - (c) removing the complementary copy of each of the template sequences from the array;
 - (d) performing a second round of sequencing of each of the immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a second complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated; and
 - (e) comparing sequences determined for the first and second complementary copy of each immobilized single-stranded template nucleic acid molecule to confirm sequencing data for each immobilized single-stranded template nucleic

acid molecule, thereby sequencing the complete genome.

36. (new) A method for sequencing nucleic acids, the method comprising:
- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm^2 ;
 - (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a first complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated, thereby performing a first round of sequencing;
 - (c) removing the complementary copy of each of the template sequences to recover an array of sequenced immobilised single-stranded template nucleic acid molecules;
 - (d) performing a second round of sequencing of each of the immobilised single-stranded template nucleic acid molecules on the recovered array of sequenced immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a second complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated; and
 - (e) comparing the first and second rounds of sequencing of each immobilized single-stranded template nucleic acid molecule to confirm sequencing data for each immobilized single-stranded template nucleic acid molecule.